SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Presnell, Scott R.
Gilbert, Teresa

(ii) TITLE OF THE INVENTION: MAMMALIAN CYTOKINE-LIKE FACTOR-7

(iii) NUMBER OF SEQUENCES: 43

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: ZymoGenetics, Inc.
(B) STREET: 1201 Eastlake Avenue East
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98102

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Lunn, Paul G
(B) REGISTRATION NUMBER: 32,743
(C) REFERENCE/DOCKET NUMBER: 97-15

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 206-442-6627
(B) TELEFAX: 206-442-6678
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 736 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 57...596
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GAATTCGGCA CGAGGAGGCG GGCAGCAGCT GCAGGCTGAC CTTGCAGCTT GGCGGA ATG      59
                                                              Met
                                                               1

GAC TGG CCT CAC AAC CTG CTG TTT CTT CTT ACC ATT TCC ATC TTC CTG     107
Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile Phe Leu
            5                  10                  15

GGG CTG GGC CAG CCC AGG AGC CCC AAA AGC AAG AGG AAG GGG CAA GGG     155
Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly
        20                  25                  30

CGG CCT GGG CCC CTG GCC CCT GGC CCT CAC CAG GTG CCA CTG GAC CTG     203
Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu
    35                  40                  45

GTG TCA CGG ATG AAA CCG TAT GCC CGC ATG GAG GAG TAT GAG AGG AAC     251
Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn
50                  55                  60                  65

ATC GAG GAG ATG GTG GCC CAG CTG AGG AAC AGC TCA GAG CTG GCC CAG     299
Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln
                70                  75                  80

AGA AAG TGT GAG GTC AAC TTG CAG CTG TGG ATG TCC AAC AAG AGG AGC     347
```

```
Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser
            85                  90                  95

CTG TCT CCC TGG GGC TAC AGC ATC AAC CAC GAC CCC AGC CGT ATC CCC      395
Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro
        100                 105                 110

GTG GAC CTG CCG GAG GCA CGG TGC CTG TGT CTG GGC TGT GTG AAC CCC      443
Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro
    115                 120                 125

TTC ACC ATG CAG GAG GAC CGC AGC ATG GTG AGC GTG CCG GTG TTC AGC      491
Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser
130                 135                 140                 145

CAG GTT CCT GTG CGC CGC CGC CTC TGC CCG CCA CCG CCC CGC ACA GGG      539
Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly
                150                 155                 160

CCT TGC CGC CAG CGC GCA GTC ATG GAG ACC ATC GCT GTG GGC TGC ACC      587
Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr
            165                 170                 175

TGC ATC TTC TGAATCACCT GGCCCAGAAG CCAGGCCAGC AGCCCGAGAC CATCCTCCT   645
Cys Ile Phe
        180

TGCACCTTTG TGCCAAGAAA GGCCTATGAA AAGTAAACAC TGACTTTTGA AAGCCAGAAA     705
AAAAAAAAAA AAAAAAAATT CCTGCGGCCG C                                    736
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile Phe
 1               5                  10                  15
Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln
            20                  25                  30
Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp
        35                  40                  45
Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg
    50                  55                  60
Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala
65                  70                  75                  80
Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg
                85                  90                  95
Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile
            100                 105                 110
Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn
        115                 120                 125
Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe
    130                 135                 140
Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr
145                 150                 155                 160
Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys
                165                 170                 175
Thr Cys Ile Phe
            180
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
AGGCGGGCAN AGCTGCAGGC TGACCTTGCA GCTTGGCGGA ATGGACTGGC CTCACAACCT     60
GCTGTTTCTT CTTACCATTT CCATCTTCCT GGGGCTGGGC AGCCAGGAGC CCCAAAAGCA    120
AGAGGAAGGG GCAAGGGCGG CCTGGGCCCN TGGCCTGGCC TCACCAGGTG CCACTGGACC    180
TGGTGTCACG GATGAAACCG TATGCCCGCA TGGAGGAGTA TGAGAGGAAC ATCGAGGAGA    240
TGGTGGCCCA GCTGAGGAAC AGCTCANAAG CTGGCCCAGA GAAAGTGTGA GGTCAACTTG    300
CAGCTGTGGA TGTCCAACAA GAAGGAGCCT GTCTCCCTTG GGGCTACAAG CATCAACCAC    360
```

CGACCCCAGC CGTATCCCCG TGGGACCTTG CCGGGAC 397

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other
(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC13265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTACCATTTC CATCTTCC 18

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other
(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC13266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCTTCCTCT TGCTTTTG 18

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC13326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAAGGATCCC AGCCCAGGAG CCCCAAAAG 29

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other
(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC13330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACCTCGAGT CAGAAGATGC AGGTGCAGCC 30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other
(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC13325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCGAATTCA TGGACTGGCC TCACAACCTG 30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other
(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC13327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAAGGATCCG AAGATGCAGG TGCAGCC 27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 692 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 50...589
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
GGGGTTCCTG GCGGGTGGCA GCTGCGGGCC TGCCGCCTGA CTTGGTGGG ATG GAC TGG     58
                                                      Met Asp Trp
                                                       1

CCG CAC AGC CTG CTC TTC CTC CTG GCC ATC TCC ATC TTC CTG GCG CCA      106
Pro His Ser Leu Leu Phe Leu Leu Ala Ile Ser Ile Phe Leu Ala Pro
    5                   10                  15

AGC CAC CCC CGG AAC ACC AAA GGC AAA AGA AAA GGG CAA GGG AGG CCC      154
Ser His Pro Arg Asn Thr Lys Gly Lys Arg Lys Gly Gln Gly Arg Pro
20                  25                  30                  35

AGT CCC TTG GCC CCT GGG CCT CAT CAG GTG CCG CTG GAC CTG GTG TCT      202
Ser Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser
                40                  45                  50

CGA GTA AAG CCC TAC GCT CGA ATG GAA GAG TAT GAG CGG AAC CTT GGG      250
Arg Val Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Leu Gly
            55                  60                  65

GAG ATG GTG GCC CAG CTG AGG AAC AGC TCC GAG CCA GCC AAG AAG AAA      298
Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Pro Ala Lys Lys Lys
        70                  75                  80

TGT GAA GTC AAT CTA CAG CTG TGG TTG TCC AAC AAG AGG AGC CTG TCC      346
Cys Glu Val Asn Leu Gln Leu Trp Leu Ser Asn Lys Arg Ser Leu Ser
    85                  90                  95

CCA TGG GGC TAC AGC ATC AAC CAC GAC CCC AGC CGC ATC CCT GCG GAC      394
Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Ala Asp
100                 105                 110                 115

TTG CCC GAG GCG CGG TGC CTA TGT TTG GGT TGC GTG AAT CCC TTC ACC      442
Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr
                120                 125                 130

ATG CAG GAG GAC CGT AGC ATG GTG AGC GTG CCA GTG TTC AGC CAG GTG      490
Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val
            135                 140                 145

CCG GTG CGC CGC CGC CTC TGT CCT CAA CCT CCT CGC CCT GGG CCC TGC      538
```

Pro Val Arg Arg Arg Leu Cys Pro Gln Pro Pro Arg Pro Gly Pro Cys
150 155 160

CGC CAG CGT GTC GTC ATG GAG ACC ATC GCT GTG GGT TGC ACC TGC ATC 586
Arg Gln Arg Val Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile
165 170 175

TTC TGAGCCAACC ACCAACCCGG TGGCCTCTGC AACAACCCTC CCTCCCTGCA CCCACT 645
Phe
180

GTGACCCTCA AGGCTGATAA ACAGTAAACG CTGTTCTTTG TAAAGGA 692

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Trp Pro His Ser Leu Leu Phe Leu Leu Ala Ile Ser Ile Phe
1 5 10 15
Leu Ala Pro Ser His Pro Arg Asn Thr Lys Gly Lys Arg Lys Gly Gln
20 25 30
Gly Arg Pro Ser Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp
35 40 45
Leu Val Ser Arg Val Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg
50 55 60
Asn Leu Gly Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Pro Ala
65 70 75 80
Lys Lys Lys Cys Glu Val Asn Leu Gln Leu Trp Leu Ser Asn Lys Arg
85 90 95
Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile
100 105 110
Pro Ala Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn
115 120 125

Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe
130 135 140
Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Gln Pro Pro Arg Pro
145 150 155 160
Gly Pro Cys Arg Gln Arg Val Val Met Glu Thr Ile Ala Val Gly Cys
165 170 175
Thr Cys Ile Phe
180

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 497 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGGGTTCCTG GCGGGTGGCA GCTGCGGGCC TGCCGCCTGA CTTGGTGGGA TGGACTGGCC 60
GCACAGCCTG CTCTTCCTCC TGGCCATCTC CATCTTCCTG GCGCCAAGCC ACCCCCGGAA 120
CACCAAAGGC AAAAGAAAAG GGCAAGGGAG GCCCAGTCCC TTGGCCCCTG GGCTCATCAG 180
GTGCCGCTGG ACCTGGTGTC TCGAGTAAAG CCCTACGCTC GAATGGAAGA GTATGAGCGG 240
AACCTTGGGG AGATGGTGGC CCAGCTGAGG AACAGCTCCG AGCCAGCCAA GAAGAAATGT 300
GAAGTCAATC TACAGCTGTG GTTGTCCAAC AAGAGGAGCC TGTCCCCATG GGGCTACAGC 360
ATCAACCACG ACCCCAGCCG CATCCCTGCG GACTTGCCCG AGGCGCGGTG CCTATGTTTG 420
GGTTGCGTGA ATCCCTTCAC CATGCAGGAG GACCGTAGCA TGGTGAGCGT GCCAGTGTTC 480
AGCCAGGTGC CGGTGCG 497

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly
1 5 10 15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
20 25 30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
35 40 45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
50 55 60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65 70 75 80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
85 90 95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
100 105 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
115 120 125
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
130 135 140
Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gln Pro Arg Ala Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly
1 5 10 15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
20 25 30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
35 40 45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
50 55 60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65 70 75 80

Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
85 90 95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
100 105 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
115 120 125
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
130 135 140
Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Pro Arg Ser Pro Lys Ala Lys Arg Lys Gly Gln Gly Arg Pro Gly
1 5 10 15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
20 25 30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
35 40 45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
50 55 60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65 70 75 80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
85 90 95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
100 105 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
115 120 125
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
130 135 140
Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Ala
 1               5                  10                  15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
            20                  25                  30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
        35                  40                  45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
    50                  55                  60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65                  70                  75                  80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
                85                  90                  95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
            100                 105                 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
        115                 120                 125
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
    130                 135                 140
Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145                 150                 155                 160
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly
1 5 10 15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ala Arg
20 25 30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
35 40 45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
50 55 60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65 70 75 80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
85 90 95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
100 105 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
115 120 125
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
130 135 140
Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly
1 5 10 15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
20 25 30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
35 40 45

Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
50 55 60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65 70 75 80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
85 90 95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
100 105 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
115 120 125
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
130 135 140
Gln Arg Val Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly
1 5 10 15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
20 25 30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
35 40 45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
50 55 60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65 70 75 80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
85 90 95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
100 105 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
115 120 125

Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
130 135 140
Gln Arg Leu Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly
1 5 10 15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
20 25 30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
35 40 45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
50 55 60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65 70 75 80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
85 90 95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
100 105 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
115 120 125
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
130 135 140
Gln Arg Phe Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly
 1               5                  10                  15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Gly Arg
            20                  25                  30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
        35                  40                  45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
    50                  55                  60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65                  70                  75                  80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
                85                  90                  95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
            100                 105                 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
        115                 120                 125
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
    130                 135                 140
Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145                 150                 155                 160
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Ser
 1               5                  10                  15
```

```
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
            20                  25                  30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
        35                  40                  45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
    50                  55                  60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65                  70                  75                  80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
                85                  90                  95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
            100                 105                 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
        115                 120                 125
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
    130                 135                 140
Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145                 150                 155                 160
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Gln Pro Arg Ser Pro Lys Val Lys Arg Lys Gly Gln Gly Arg Pro Gly
 1               5                  10                  15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
            20                  25                  30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
        35                  40                  45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
    50                  55                  60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65                  70                  75                  80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
                85                  90                  95
```

```
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
            100                 105                 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
        115                 120                 125
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
    130                 135                 140
Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145                 150                 155                 160
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Gln Pro Arg Val Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly
 1               5                  10                  15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
            20                  25                  30
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
        35                  40                  45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
    50                  55                  60
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65                  70                  75                  80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
                85                  90                  95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
            100                 105                 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
        115                 120                 125
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
    130                 135                 140
Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145                 150                 155                 160
```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser
 1               5                  10                  15
Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp
            20                  25                  30
Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr
        35                  40                  45
Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val
    50                  55                  60
Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys
65                  70                  75                  80
Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile
                85                  90                  95
Phe
```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly Pro
 1               5                  10                  15
Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg Met
            20                  25                  30
Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu Met
        35                  40                  45
```

Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu
50 55 60
Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp
65 70 75 80
Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro
85 90 95
Glu Ala Arg Cys
100

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly Pro
1 5 10 15
Leu

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu
1 5 10 15
Glu

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg Cys
 1               5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys
 1               5                  10                  15
Arg Gln Arg
```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly Pro
 1               5                  10                  15
```

Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg Met
20 25 30
Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu
1 5 10 15
Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys
20 25 30
Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser
35 40 45
Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp
50 55 60
Leu Pro Glu Ala Arg Cys
65 70

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg Cys
1 5 10 15

Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp Arg Ser
20 25 30
Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg Arg Arg Leu
35 40 45
Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg Cys
1 5 10 15
Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp Arg Ser
20 25 30
Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg Arg Arg Leu
35 40 45
Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln Arg Ala Val Met
50 55 60
Glu Thr Ile Ala Val Gly Cys Thr Cys
65 70

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly Pro Leu
1 5 10 15
Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg Met Lys
20 25 30
Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu Met Val
35 40 45
Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val
50 55 60
Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly
65 70 75 80
Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu
85 90 95
Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu
100 105 110
Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
115 120 125
Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln Arg
130 135 140
Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145 150 155

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro
1 5 10 15
His Gln Val Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg
20 25 30
Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg
35 40 45
Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
50 55 60
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn
65 70 75 80

His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu
85 90 95
Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met
100 105 110
Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys
115 120 125
Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln Arg Ala Val Met Glu
130 135 140
Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145 150

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Lys Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
1 5 10 15
Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu
20 25 30
Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser
35 40 45
Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser
50 55 60
Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro
65 70 75 80
Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly
85 90 95
Cys Val Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val
100 105 110
Pro Val Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro
115 120 125
Pro Arg Thr Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala
130 135 140
Val Gly Cys Thr Cys Ile Phe
145 150

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
His Pro Arg Asn Thr Lys Gly Lys Arg Lys Gly Gln Gly Arg Pro Ser
 1               5                  10                  15
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
            20                  25                  30
Val Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Leu Gly Glu
        35                  40                  45
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Pro Ala Lys Lys Lys Cys
    50                  55                  60
Glu Val Asn Leu Gln Leu Trp Leu Ser Asn Lys Arg Ser Leu Ser Pro
65                  70                  75                  80
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Ala Asp Leu
                85                  90                  95
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
            100                 105                 110
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
        115                 120                 125
Val Arg Arg Arg Leu Cys Pro Gln Pro Pro Arg Pro Gly Pro Cys Arg
    130                 135                 140
Gln Arg Val Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145                 150                 155                 160
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```
Arg Asn Thr Lys Gly Lys Arg Lys Gly Gln Gly Arg Pro Ser Pro Leu
 1               5                  10                  15
Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg Val Lys
            20                  25                  30
Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Leu Gly Glu Met Val
        35                  40                  45
Ala Gln Leu Arg Asn Ser Ser Glu Pro Ala Lys Lys Lys Cys Glu Val
    50                  55                  60
Asn Leu Gln Leu Trp Leu Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly
65                  70                  75                  80
Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Ala Asp Leu Pro Glu
                85                  90                  95
Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu
            100                 105                 110
Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
        115                 120                 125
Arg Arg Leu Cys Pro Gln Pro Pro Arg Pro Gly Pro Cys Arg Gln Arg
    130                 135                 140
Val Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```
Lys Arg Lys Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His
 1               5                  10                  15
Gln Val Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met
            20                  25                  30
Glu Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
        35                  40                  45
```

Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp
    50   55   60
Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His
65   70   75   80
Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys
                85   90   95
Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val
            100   105   110
Ser Val Pro Val Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro
        115   120   125
Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr
    130   135   140
Ile Ala Val Gly Cys Thr Cys Ile Phe
145   150

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
 1   5   10   15
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
            20   25   30
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
        35   40   45
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
    50   55   60
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
65   70   75   80
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
                85   90   95
Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
            100   105   110
Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
        115   120   125

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly Pro Leu
 1               5                  10                  15
Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg Met Lys
            20                  25                  30
Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu Met Val
        35                  40                  45
Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val
    50                  55                  60
Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly
65                  70                  75                  80
Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu
                85                  90                  95
Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu
            100                 105                 110
Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
        115                 120                 125
Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln Arg
    130                 135                 140
Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile
145                 150                 155
```